

Package ‘sprsmdl’

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Title Sparse modeling toolkit

Type Package

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Description R functions to mine sparse models from data.

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sprsm1-package *Sparse modeling toolkit*

Description

R functions to mine sparse models from data.

Details

Providing functions to find few but significant variables that can explain data well.

Author(s)

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SlrArd *Sparse Logistic Regression*

Description

Sparse logistic regression (SLR) with automatic relevance determination (ARD).

Usage

```
SlrArd(T, X, bias = TRUE, method = c("VB", "VBMackay", "PX-VB"), control = list(), check.lb=TRUE, a0 =
```

Arguments

T	A vector of binary categorical dependent variable.
X	A matrix, each row of which is a vector of independent variables.
bias	A logical value specifying whether to include intercept or not.
method	The method to be used. See ‘Details’.
control	A list of control parameters. See ‘Details’.
check.lb	A logical value whether to check the validity of parameter updates. Defaults to TRUE.
	Hyper parameters:
a0	Shape of Gamma distribution.
b0	Rate of Gamma distribution.
	Initial values:
mu0	Coefficients.
xi0	Variational parameter.

Details

Some independent variables can be pruned in each VB-EM iteration and never be used for successive iterations when irrelevance of the variables exceed a threshold determined by `control$pruning`. Explicitly set `control$pruning = Inf` to prevent the pruning.

Method `"VB"` is a variational Bayesian method that is robust. See Bishop (2006).

Method `"VBMacKay"` is basically same as `"VB"` but some parameters are updated based on method of MacKay (1992). Global convergence has not been proven but this algorithm will be faster.

Method `"PX-VB"` based on the Parameter eXpanded VB method proposed in Qi and Jaakkola (2007). Global convergence is proven and could be faster than `"VB"`.

The control argument is a list that can supply any of the following components:

- `pruning`: threshold of independent variables pruning. No variables are pruned if `'Inf'`. Defaults to `'1e+8'`.

See `?optim` for meanings of the following control parameters.

- `maxit`: Defaults to `'10^5'`.
- `reltol`: Defaults to `'sqrt(.Machine$double.eps)'`.
- `trace`: Defaults to `'TRUE'`.
- `REPORT`: Defaults to `'floor(control$maxit / 20)'`.

Value

<code>coefficients</code>	A named vector of coefficients.
<code>irrelevance</code>	A named vector of irrelevance.
<code>iterations</code>	A number of iterations.
<code>converged</code>	A logical value giving whether the iterations converged or not.
<code>lower.bound</code>	The lower bound of the marginal log-likelihood minus a constant term.
<code>method</code>	The method used.
<code>lb.diff</code>	The difference of the lower bounds in each update. This exists when <code>check.lb = TRUE</code> .
<code>fitted.values</code>	The fitted values.
<code>residuals</code>	The residuals, that is T minus fitted values.

Author(s)

Hiroshi Saito <die.saito@gmail.com>

References

Bishop, C. M. (2006) Pattern recognition and machine learning. Springer.

MacKay, D. J. C. (1992) Bayesian interpolation. *Neural Computation*, *4*(3), 415-447.

Qi, Y. and Jaakkola, T. S. (2007) Parameter expanded variational Bayesian methods. *Advances in Neural Information Processing Systems*, *19*, 1097.

Examples

```
data(iris)

tmp <- iris[iris$Species != 'versicolor',]
T <- tmp$Species == 'setosa'
X <- as.matrix(tmp[,1:4])

res <- SlrArd(T, X, bias=TRUE, method="VB", control = list(maxit=500))
print(coefficients(res))

res <- SlrArd(T, X, bias=TRUE, method="VBMackKay") ## faster
print(coefficients(res))

res <- SlrArd(T, X, bias=FALSE, method="VBMackKay") ## without bias
print(coefficients(res))
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